

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	PLAG1 and CTNNB1	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:37
L2	17	PLAG1	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:38
L3	50	CTNNB1 and (cancer\$3 tumor\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:38
L4	1	I3 and (CTNNB1 near5 fus\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:39
L5	1	(CTNNB1 near5 fus\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:39
L6	21	(beta adj1 catenin) near5 fus\$3	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:40
L7	14	((beta adj1 catenin) CTNNB1) near5 (exon)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:41

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:54:54 ; Search time 30170 Seconds
(without alignments)
11745.210 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgcc 7313

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
	1	7313	100.0	7313	9	HSU65002 U65002 Human zinc
	2	7262	99.3	7313	6	A69511 A69511 Sequence 1
c	3	5728	78.3	142102	9	AC107952 AC107952 Homo sapi
	4	1514	20.7	1565	9	BC075047 BC075047 Homo sapi
	5	1514	20.7	1565	9	BC075048 BC075048 Homo sapi
	6	687	9.4	65748	2	AC090187 AC090187 Homo sapi
	7	601	8.2	49357	2	AC107961 AC107961 Homo sapi
c	8	420	5.7	65748	2	AC090187 AC090187 Homo sapi
c	9	406	5.6	421	11	G25280 G25280 human STS E

						Untitled	
c	10	381	5.2	550	9	AF221550	AF221550 Homo sapi
c	11	315	4.3	376	6	AR274991	AR274991 Sequence
c	12	225	3.1	274	9	AF221549	AF221549 Homo sapi
c	13	177	2.4	177	11	G33002	G33002 A009Z02 Hum
c	14	119	1.6	524	9	AF221548	AF221548 Homo sapi
c	15	117	1.6	3161	10	AY574219	AY574219 Mus muscu
c	16	117	1.6	182102	2	AC097274	AC097274 Mus muscu
c	17	117	1.6	241148	10	AL807387	AL807387 Mouse DNA
c	18	110	1.5	49357	2	AC107961	AC107961 Homo sapi
c	19	100	1.4	201	11	BV200913	BV200913 sqnm20538
c	20	98	1.3	135	9	HSU78783	U78783 Human tumor
c	21	80	1.1	278377	2	AC129839	AC129839 Rattus no
c	22	78	1.1	1575	10	AF057366	AF057366 Mus muscu
c	23	66	0.9	244955	2	AC123210	AC123210 Rattus no
c	24	60	0.8	60	6	CQ543597	CQ543597 Sequence
c	25	50	0.7	1381	5	CR406846	CR406846 Gallus ga
c	26	45	0.6	66	11	HSU84997	U84997 Homo sapien
c	27	39	0.5	107	5	CR353258	CR353258 Gallus ga
c	28	36	0.5	176067	10	AC129040	AC129040 Rattus no
c	29	36	0.5	185673	2	AC141142	AC141142 Rattus no
c	30	35	0.5	660	6	AR502666	AR502666 Sequence
c	31	35	0.5	660	6	AR517948	AR517948 Sequence
c	32	35	0.5	160726	9	AC092421	AC092421 Homo sapi
c	33	35	0.5	172947	2	AC068813	AC068813 Homo sapi
c	34	35	0.5	173037	2	AC018542	AC018542 Homo sapi
c	35	35	0.5	179190	9	AC114477	AC114477 Homo sapi
c	36	35	0.5	194609	2	AC013775	AC013775 Mus muscu
c	37	35	0.5	207086	10	AL596117	AL596117 Mouse DNA
c	38	35	0.5	228232	2	AC090293	AC090293 Mus muscu
c	39	34	0.5	728	10	BC031746	BC031746 Mus muscu
c	40	34	0.5	752	8	AY125589	AY125589 Cylindrot
c	41	34	0.5	840	3	AY089459	AY089459 Drosophil
c	42	34	0.5	1900	9	BC071628	BC071628 Homo sapi
c	43	34	0.5	2192	5	BC063223	BC063223 Xenopus t
c	44	34	0.5	3440	10	BC047268	BC047268 Mus muscu
c	45	34	0.5	3911	8	AY639654	AY639654 Pinus rad

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:37:20 ; Search time 3456 Seconds
(without alignments)
12526.351 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcggtgcc 7313

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
c 1	7262	99.3	7313	2	AAV29268	Aav29268 Nucleotid
c 2	315	4.3	376	10	ADB31412	Adb31412 Testoster
c 3	117	1.6	4050	12	ADO35615	Ado35615 Novel mou
c 4	117	1.6	24348	11	ACN44976	Acn44976 Mouse gen
5	72	1.0	72	4	AAS13082	Aas13082 DNA encod
6	72	1.0	72	8	ACC41633	Acc41633 Human zin
7	60	0.8	60	6	ABN40484	Abn40484 Human spl
8	35	0.5	24127	11	ACN44540	Acn44540 Mouse gen
c 9	34	0.5	540	10	ABX57327	Abx57327 Arabidops
10	34	0.5	3463	3	AAA40241	Aaa40241 Pig heart

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11	33	0.5	261	12	ADQ18288		Adq18288	Human sof
12	33	0.5	330	12	ADQ20280		Adq20280	Human sof
c 13	33	0.5	360	6	ABQ85662		Abq85662	Arabidops
c 14	33	0.5	372	5	ABV37528		Abv37528	Human pro
c 15	33	0.5	385	10	ABX61502		Abx61502	Arabidops
16	33	0.5	413	4	AAI85388		Aai85388	Human pol
17	33	0.5	479	13	ACN52747		Acn52747	Cotton an
c 18	33	0.5	483	13	ACN47280		Acn47280	Cotton pr
19	33	0.5	512	9	ACH26480		Ach26480	Human adu
20	33	0.5	523	13	ACN58184		Acn58184	Cotton gy
21	33	0.5	945	10	ADL18516		Adl18516	Rice glut
22	33	0.5	1034	6	ABK65255		Abk65255	Arabidops
23	33	0.5	1034	10	ADD29974		Add29974	Plant yie
24	33	0.5	1034	12	ADI41806		Adi41806	Plant tra
25	33	0.5	1335	3	AAA47331		Aaa47331	FtsZ homo
26	33	0.5	1372	12	ADQ22819		Adq22819	Human sof
27	33	0.5	1372	12	ADQ22824		Adq22824	Human sof
28	33	0.5	1510	4	AAD08081		Aad08081	Rice oleo
29	33	0.5	1832	5	ADL63631		Adl63631	Human ova
30	33	0.5	2206	4	ABK43595		Abk43595	DNA encod
31	33	0.5	2206	12	ADI53982		Adi53982	cdNA enco
32	33	0.5	2385	4	ABL15036		Ab115036	Drosophil
c 33	33	0.5	2398	3	AAZ37263		Aaz37263	SGRF codi
34	33	0.5	2540	6	ABQ73251		Abq73251	Human MAP
35	33	0.5	2823	4	AAS34806		Aas34806	cdNA enco
36	33	0.5	2823	10	ADC45964		Adc45964	Human neo
37	33	0.5	8447	6	ABN80093		Abn80093	Human che
c 38	32	0.4	51	4	AAL28293		Aal28293	Human SNP
39	32	0.4	163	5	ABV58311		Abv58311	Human pro
40	32	0.4	204	5	ABV57555		Abv57555	Human pro
41	32	0.4	312	5	ABV49552		Abv49552	Human pro
c 42	32	0.4	341	10	ABX61217		Abx61217	Arabidops
43	32	0.4	348	4	AAI80658		Aai80658	Human pol
c 44	32	0.4	389	5	ABV61698		Abv61698	Human pro
45	32	0.4	397	4	AAI86207		Aai86207	Human pol

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:06:47 ; Search time 3852 Seconds
(without alignments)
11784.990 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgcc 7313

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 6054689 seqs, 3103772919 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Page 1

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Result No.	Score	Query Match	Length	DB	ID	Description
	1	7313	100.0	7313	9	US-09-242-772-116
c	2	315	4.3	376	21	US-10-831-704-128
c	3	117	1.6	24348	13	US-10-087-192-1693
	4	72	1.0	72	9	US-09-785-632A-136
	5	72	1.0	72	16	US-10-223-765-136
	6	60	0.8	60	10	US-09-908-975-13232
	7	35	0.5	240	18	US-10-424-599-118528
c	8	35	0.5	671	20	US-10-425-115-64671
	9	35	0.5	735	20	US-10-425-115-17914
	10	35	0.5	3112	20	US-10-425-115-51136
	11	35	0.5	24127	13	US-10-087-192-1039
	12	34	0.5	470	19	US-10-437-963-45935
c	13	34	0.5	540	9	US-09-770-152-679
c	14	34	0.5	2124	18	US-10-424-599-3238
	15	33	0.5	197	20	US-10-425-115-36720
	16	33	0.5	261	20	US-10-723-860-1106
	17	33	0.5	270	19	US-10-437-963-6529
	18	33	0.5	282	20	US-10-425-115-134998
	19	33	0.5	330	20	US-10-723-860-3100
c	20	33	0.5	345	20	US-10-425-115-31440
c	21	33	0.5	360	9	US-09-770-791-532
c	22	33	0.5	372	20	US-10-357-930-37547
	23	33	0.5	375	20	US-10-425-115-165833
	24	33	0.5	380	20	US-10-425-115-57654
	25	33	0.5	384	18	US-10-424-599-58174
c	26	33	0.5	385	9	US-09-924-035A-848
c	27	33	0.5	392	20	US-10-425-115-65919
c	28	33	0.5	402	18	US-10-424-599-76918
	29	33	0.5	422	20	US-10-425-115-89893
c	30	33	0.5	427	20	US-10-425-115-4382
	31	33	0.5	430	20	US-10-425-115-58879
c	32	33	0.5	458	19	US-10-437-963-86639
c	33	33	0.5	465	19	US-10-437-963-34432
	34	33	0.5	479	19	US-10-021-323-7528
c	35	33	0.5	483	19	US-10-021-323-2061
c	36	33	0.5	484	18	US-10-424-599-92471
	37	33	0.5	512	10	US-09-918-995-13692
	38	33	0.5	523	19	US-10-021-323-12965
c	39	33	0.5	570	20	US-10-425-115-48090
c	40	33	0.5	626	20	US-10-425-115-14398
c	41	33	0.5	637	20	US-10-425-115-33996
c	42	33	0.5	690	20	US-10-425-115-164109
	43	33	0.5	715	21	US-10-956-157-3705
	44	33	0.5	715	21	US-10-956-157-8940
c	45	33	0.5	787	20	US-10-425-115-126784

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 01:23:31 ; Search time 3482 Seconds
(without alignments)
9277.886 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggtagcgatataactacaat.....tatgaataaaatctcggtcc 7313

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 12999316 seqs, 2208778887 residues

word size : 0

Total number of hits satisfying chosen parameters: 25998632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*

3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*

9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*

10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*

11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*

12: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*

13: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*

14: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*

15: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	563	7.7	4174	15	US-60-680-544-32916	Sequence 32916, A
2	563	7.7	4174	15	US-60-680-473-32916	Sequence 32916, A
3	35	0.5	760	9	US-10-703-032-103073	Sequence 103073,
c 4	34	0.5	601	11	US-10-940-774A-28962	Sequence 28962, A
c 5	34	0.5	601	11	US-10-940-774A-125909	Sequence 125909,
c 6	34	0.5	115963	11	US-10-940-774A-12298	Sequence 12298, A
c 7	34	0.5	144322	11	US-10-940-774A-15316	Sequence 15316, A
c 8	34	0.5	152321	15	US-60-659-397-12128	Sequence 12128, A

Untitled

c	9	33	0.5	201	11	US-10-990-328A-541037	Sequence 541037,
c	10	33	0.5	400	9	US-10-703-032-73280	Sequence 73280, A
c	11	33	0.5	400	9	US-10-703-032-99398	Sequence 99398, A
c	12	33	0.5	450	9	US-10-703-032-79323	Sequence 79323, A
c	13	33	0.5	456	9	US-10-703-032-70659	Sequence 70659, A
c	14	33	0.5	496	9	US-10-703-032-88434	Sequence 88434, A
c	15	33	0.5	601	11	US-10-940-774A-115142	Sequence 115142,
c	16	33	0.5	696	9	US-10-703-032-13726	Sequence 13726, A
c	17	33	0.5	732	9	US-10-703-032-12833	Sequence 12833, A
c	18	33	0.5	766	9	US-10-703-032-17311	Sequence 17311, A
c	19	33	0.5	1034	6	US-09-713-994A-1780	Sequence 1780, Ap
c	20	33	0.5	1747	7	US-10-062-254A-357	Sequence 357, App
c	21	33	0.5	2385	12	US-11-097-143-19795	Sequence 19795, A
c	22	33	0.5	11730	11	US-10-940-774A-14991	Sequence 14991, A
c	23	33	0.5	29571	15	US-60-659-397-12103	Sequence 12103, A
c	24	33	0.5	49416	11	US-10-940-774A-15234	Sequence 15234, A
c	25	33	0.5	93364	11	US-10-940-774A-14890	Sequence 14890, A
c	26	33	0.5	151541	11	US-10-990-328A-97855	Sequence 97855, A
c	27	33	0.5	283538	11	US-10-940-774A-13506	Sequence 13506, A
c	28	33	0.5	401433	2	PCT-US04-42189-79	Sequence 79, Appl
c	29	33	0.5	474412	11	US-10-990-328A-98016	Sequence 98016, A
c	30	33	0.5	483207	1	PCT-US04-37982-3303	Sequence 3303, Ap
c	31	32	0.4	51	6	US-09-749-280D-1501	Sequence 1501, Ap
c	32	32	0.4	201	11	US-10-990-328A-215196	Sequence 215196,
c	33	32	0.4	201	11	US-10-990-328A-215230	Sequence 215230,
c	34	32	0.4	201	11	US-10-990-328A-234783	Sequence 234783,
c	35	32	0.4	201	11	US-10-990-328A-234784	Sequence 234784,
c	36	32	0.4	446	9	US-10-703-032-3773	Sequence 3773, Ap
c	37	32	0.4	525	15	US-60-680-544-3950	Sequence 3950, Ap
c	38	32	0.4	525	15	US-60-680-544-14578	Sequence 14578, A
c	39	32	0.4	525	15	US-60-680-473-3950	Sequence 3950, Ap
c	40	32	0.4	525	15	US-60-680-473-14578	Sequence 14578, A
c	41	32	0.4	564	9	US-10-703-032-57200	Sequence 57200, A
c	42	32	0.4	600	13	US-11-060-756-278	Sequence 278, App
c	43	32	0.4	600	13	US-11-060-756-4550	Sequence 4550, Ap
c	44	32	0.4	784	7	US-10-456-882A-40	Sequence 40, Appl
c	45	32	0.4	830	15	US-60-680-544-17295	Sequence 17295, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 11:48:05 ; Search time 21091 Seconds
(without alignments)
13198.236 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcggtgcc 7313

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
c 1	1452	19.9	1503	9	AY420150	AY420150 Homo sapi
c 2	685	9.4	693	4	BM724590	BM724590 UI-E-E01-
c 3	679	9.3	1503	9	AY420151	AY420151 Pan trogl
c 4	637	8.7	742	6	CA413047	CA413047 UI-H-EZ0-
c 5	596	8.1	864	5	BX370812	BX370812 BX370812
c 6	583	8.0	583	5	BP317766	BP317766 BP317766
c 7	570	7.8	570	2	AW339499	AW339499 xz91g05.x
c 8	548	7.5	734	6	CA411972	CA411972 UI-H-EZ0-
c 9	541	7.4	616	5	BU686683	BU686683 UI-CF-DU1
c 10	540	7.4	540	1	AA706806	AA706806 zj30c09.s
c 11	518	7.1	518	2	BF115791	BF115791 7n64h11.x
c 12	514	7.0	1047	5	BX402039	BX402039 BX402039
c 13	497	6.8	500	2	BF507694	BF507694 UI-H-BW1-
c 14	497	6.8	736	1	AL036879	AL036879 DKFZp564P

Untitled

c 15	487	6.7	1165	5	BX424854	BX424854	BX424854
c 16	482	6.6	482	1	AA707386	AA707386	zj27e09.s
c 17	475	6.5	790	1	AU138448	AU138448	AU138448
c 18	464	6.3	466	1	AA628501	AA628501	af27d06.s
c 19	461	6.3	909	5	BU181917	BU181917	AGENCOURT
c 20	459	6.3	467	2	AW274762	AW274762	xn34h01.x
c 21	448	6.1	597	2	AW977860	AW977860	EST389864
c 22	439	6.0	449	6	CA771364	CA771364	io70c07.y
c 23	438	6.0	907	4	BG613583	BG613583	602641935
c 24	430	5.9	432	2	BF432133	BF432133	nab79g01.
c 25	426	5.8	536	7	CN410058	CN410058	170004245
c 26	423	5.8	423	1	AI334157	AI334157	qq07h12.x
c 27	409	5.6	458	2	AW002999	AW002999	wq62d08.x
c 28	409	5.6	560	1	AI808840	AI808840	wf97h04.x
c 29	406	5.6	421	7	D59273	D59273	HUM007A10A
c 30	373	5.1	373	1	AA418372	AA418372	zv96g12.r
c 31	373	5.1	494	2	AW007402	AW007402	wt55b04.x
c 32	371	5.1	569	5	BP379355	BP379355	BP379355
c 33	353	4.8	427	1	AI223324	AI223324	qg71c02.x
c 34	347	4.7	391	7	N95376	N95376	zb71f10.s1
c 35	320	4.4	460	1	AV745206	AV745206	AV745206
c 36	315	4.3	673	9	AG120959	AG120959	Pan_trogl
c 37	310	4.2	514	7	CN410057	CN410057	170005830
c 38	305	4.2	467	7	T83418	T83418	yd44d05.r1
c 39	299	4.1	410	7	CN410056	CN410056	170005325
c 40	288	3.9	319	2	AW138020	AW138020	UI-H-BI1-
c 41	285	3.9	517	7	T81600	T81600	yd44d05.s1
c 42	284	3.9	489	1	AV745506	AV745506	AV745506
c 43	261	3.6	454	1	AA418251	AA418251	zv96c12.s
c 44	259	3.5	259	1	AA421591	AA421591	zu25f01.r
c 45	249	3.4	922	4	BG253502	BG253502	602364227